



SEQUENCE LISTING

<110> Munroe, Donald  
Gupta, Ashwani  
Vyas, Tejal  
Chun, Jerold

<120> MAMMALIAN EDG-5 RECEPTOR HOMOLOGS

<130> 2931-105 (new); P108074-00003 (old)

<140> US 09/581252  
<141> 2000-12-04

<150> PCT/CA 98/01193  
<151> 1998-12-24

<150> US 08/997803  
<151> 1997-12-24

<160> 28

<170> PatentIn version 3.2

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33

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<210> 4  
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37

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 atgctggctgc atagcaacct gaccaaaaag 30

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<210> 8  
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<210> 9  
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 <212> DNA  
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<210> 11  
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<400> 11  
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<210> 12  
 <211> 1523  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Nucleotide sequence of the genomic DNA flanking 5' end of the  
 hedg-5 cDNA insert of pC3-hedg-55 clone and the hedg-5 cDNA

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cgggcctggg ggttctgccc ctcgacggcc tgaactgcag gcagtgtggc gtgcagcatg	1080
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cctacaagga cgaggacatg tatggcacca tgaagaagat gatctgctgc ttctctcagg	1200
agaaccacaga gaggcgtccc tctcgcatcc cctccacagt cctcagcagg agtgacacag	1260
gcagccagta catagaggat agtattagcc aagggtgcagt ctgcaataaa agcacttct	1320
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attacctgtc tctaacaaag cccatgtaca gtgttatttg aggtctccat taatcactgc	1440
tagatttctt taaaaaattt tttttcatag tttaaaagca tgggcagtaa agagaggacc	1500
tgctgcattt agagaaagca cag	1523

<210> 13  
 <211> 1357  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Nucleotide sequence of a hEDG-5 cDNA inserted into pcDNA3

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acatggactt tttttataat aggagcaaca ctgatactgt cgatgactgg acaggaacaa	120
agcttgtgat tgttttgtgt gttgggacgt ttttctgcct gtttattttt ttttctaatt	180
ctctggtcac cgcggcagtg atcaaaaaca gaaaatttca tttccccttt tactacctgt	240
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acacaggccc agtttcaaaa actttgactg tcaaccgctg gtttctccgt caggggcttc 360  
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 gtggcgctgca gcatgtgaaa aggtgggttc tgctgctggc gctgctcaac tccgtcgtga 900  
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<210> 14

<211> 353

<212> PRT

<213> Artificial Sequence

<220>

<223> Predicted amino acid sequence of pC3-hedg5-3 clone

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			20					25					30		

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 35 40 45  
 Ser Leu Val Ile Ala Ala Val Ile Lys Asn Arg Lys Phe His Phe Pro  
 50 55 60  
 Phe Tyr Tyr Leu Leu Ala Asn Leu Ala Ala Asp Phe Phe Ala Gly  
 65 70 75 80  
 Ile Ala Tyr Val Phe Leu Met Phe Asn Thr Gly Pro Val Ser Lys Thr  
 85 90 95  
 Leu Thr Val Asn Arg Trp Phe Leu Arg Gln Gly Leu Leu Asp Ser Ser  
 100 105 110  
 Leu Thr Ala Ser Leu Thr Asn Leu Leu Val Ile Ala Val Glu Arg His  
 115 120 125  
 Met Ser Ile Met Arg Met Arg Val His Ser Asn Leu Thr Lys Lys Arg  
 130 135 140  
 Val Thr Leu Leu Ile Leu Leu Val Trp Ala Ile Ala Ile Phe Met Gly  
 145 150 155 160  
 Ala Val Pro Thr Leu Gly Trp Asn Cys Leu Cys Asn Ile Ser Ala Cys  
 165 170 175  
 Ser Ser Leu Ala Pro Ile Tyr Ser Arg Ser Tyr Leu Val Phe Trp Thr  
 180 185 190  
 Val Ser Asn Leu Met Ala Phe Leu Ile Met Val Val Val Tyr Leu Arg  
 195 200 205  
 Ile Tyr Val Tyr Val Lys Arg Lys Thr Asn Val Leu Ser Pro His Thr  
 210 215 220  
 Ser Gly Ser Ile Ser Arg Arg Arg Thr Pro Met Lys Leu Met Lys Thr  
 225 230 235 240  
 Val Met Thr Val Leu Gly Ala Phe Val Val Cys Trp Thr Pro Gly Leu  
 245 250 255

Val Val Leu Pro Leu Asp Gly Leu Asn Cys Arg Gln Cys Gly Val Gln  
260 265 270

His Val Lys Arg Trp Phe Leu Leu Leu Ala Leu Leu Asn Ser Val Val  
275 280 285

Asn Pro Ile Ile Tyr Ser Tyr Lys Asp Glu Asp Met Tyr Gly Thr Met  
290 295 300

Lys Lys Met Ile Cys Cys Phe Ser Gln Glu Asn Pro Glu Arg Arg Pro  
305 310 315 320

Ser Arg Ile Pro Ser Thr Val Leu Ser Arg Ser Asp Thr Gly Ser Gln  
325 330 335

Tyr Ile Glu Asp Ser Ile Ser Gln Gly Ala Val Cys Asn Lys Ser Thr  
340 345 350

Ser

<210> 15

<211> 213

<212> PRT

<213> Artificial Sequence

<220>

<223> Predicted amino acid sequence of mouse partial EDG-5 cDNA

<220>

<221> MISC\_FEATURE

<222> (188)..(210)

<223> Xaa = unknown

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1 5 10 15

Arg Gln Gly Leu Leu Asp Thr Ser Leu Thr Ala Ser Leu Ala Asn Leu  
20 25 30

Leu Val Ile Ala Val Glu Arg His Met Ser Ile Met Arg Met Arg Val



35

40

45

His Ser Asn Leu Thr Lys Lys Arg Val Thr Leu Leu Ile Leu Leu Val  
50 55 60

Trp Ala Ile Ala Ile Phe Met Gly Ala Val Pro Thr Leu Gly Trp Asn  
65 70 75 80

Cys Leu Cys Asn Ile Ser Ala Cys Ser Ser Leu Ala Pro Ile Tyr Ser  
85 90 95

Arg Ser Tyr Leu Ile Phe Trp Thr Val Ser Asn Leu Leu Ala Phe Phe  
100 105 110

Ile Met Val Ala Val Tyr Val Arg Ile Tyr Met Tyr Val Lys Arg Lys  
115 120 125

Thr Asn Val Leu Ser Pro His Thr Ser Gly Ser Ile Ser Arg Arg Arg  
130 135 140

Ala Pro Met Lys Leu Met Lys Thr Val Met Thr Val Leu Gly Ala Phe  
145 150 155 160

Val Val Cys Trp Thr Pro Gly Leu Val Val Leu Leu Leu Asp Gly Leu  
165 170 175

Asn Cys Lys Gln Cys Asn Val Gln His Val Lys Xaa Trp Phe Leu Leu  
180 185 190

Leu Ala Leu Leu Asn Ser Val Met Asn Pro Leu Ile Tyr Cys Arg Ser  
195 200 205

Pro Xaa Phe Pro Trp  
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<210> 16  
<211> 24  
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<210> 19  
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 <223> PCR primer: HE5-1322R

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<213> Artificial Sequence

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<223> PCR primer: HE5-Kpn1322R

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39

<210> 22

<211> 2033

<212> DNA

<213> Artificial Sequence

<220>

<223> Full length mEDG-5 cDNA

<400> 22

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aacaggagca acacagacac agcggacgag tggacaggga caaagcttgt gatcgctcctg 120

tgcgtgggga cgttcttctg cctctttata ttttttctta actccctggg cattgctgcg 180

gtgatcaca accggaagtt ccactttccc ttctactacc tgctggctaa cttagctgct 240

gcggtattct tcgccggaat cgcttacgtg ttctgatgt ttaacactgg cccggtgtcg 300

aaaacgttga ccgtcaaccg ctggttcctc cgccaggggc tcctagacac cagcctgact 360

gcctccctgg ccaatttgct gggtattgct gtggaaagac acatgtcaat catgaggatg 420

agagtccaca gcaacttgac caaaaagcgg gtgacgctgc tcattctgct ggtgtgggcc 480

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aggaaaacca acgtcttata tccacacacc agtggctcca tcagccgccg gagggctccc 720

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aagcgtggt tcctgctgct cgcactgctc aactccgtca tgaaccccat catctactcg 900

tacaaggacg aggacatgta caacaccatg cggaagatga tctgctgtgc cctgcaggac 960

agcaataaccg agaggcgccc ctcccgcaac ccctccacca tccacagcag gagcgagacg 1020

ggcagccagt acctggagga cagcatcagc cagggcccgg tgtgcaataa aaacggctcc 1080

taagccacgg acgcctccgc cctcttcccc tggggaaaga gctgttaagc gtcctcacct 1140

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<210> 23
<211> 354
<212> PRT
<213> Mouse

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<400> 23

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          20          25          30

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Val Leu Cys Val Gly Thr Phe Phe Cys Leu Phe Ile Phe Phe Ser Asn
          35          40          45

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Ser Leu Val Ile Ala Ala Val Ile Thr Asn Arg Lys Phe His Phe Pro
          50          55          60

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Ile Ala Tyr Val Phe Leu Met Phe Asn Thr Gly Pro Val Ser Lys Thr  
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Leu Thr Val Asn Arg Trp Phe Leu Arg Gln Gly Leu Leu Asp Thr Ser  
100 105 110  
Leu Thr Ala Ser Leu Ala Asn Leu Leu Val Ile Ala Val Glu Arg His  
115 120 125  
Met Ser Ile Met Arg Met Arg Val His Ser Asn Leu Thr Lys Lys Arg  
130 135 140  
Val Thr Leu Leu Ile Leu Leu Val Trp Ala Ile Ala Ile Phe Met Gly  
145 150 155 160  
Ala Val Pro Thr Leu Gly Trp Asn Cys Leu Cys Asn Ile Ser Ala Cys  
165 170 175  
Ser Ser Leu Ala Pro Ile Tyr Ser Arg Ser Tyr Leu Ile Phe Trp Thr  
180 185 190  
Val Ser Asn Leu Leu Ala Phe Phe Ile Met Val Ala Val Tyr Val Arg  
195 200 205  
Ile Tyr Met Tyr Val Lys Arg Lys Thr Asn Val Leu Ser Pro His Thr  
210 215 220  
Ser Gly Ser Ile Ser Arg Arg Arg Ala Pro Met Lys Leu Met Lys Thr  
225 230 235 240  
Val Met Thr Val Leu Gly Ala Phe Val Val Cys Trp Thr Pro Gly Leu  
245 250 255  
Val Val Leu Leu Leu Asp Gly Leu Asn Cys Lys Gln Cys Asn Val Gln  
260 265 270  
His Val Lys Arg Trp Phe Leu Leu Leu Ala Leu Leu Asn Ser Val Met  
275 280 285

Asn Pro Ile Ile Tyr Ser Tyr Lys Asp Glu Asp Met Tyr Asn Thr Met  
 290 295 300

Arg Lys Met Ile Cys Cys Ala Leu Gln Asp Ser Asn Thr Glu Arg Arg  
 305 310 315 320

Pro Ser Arg Asn Pro Ser Thr Ile His Ser Arg Ser Glu Thr Gly Ser  
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Gln Tyr Leu Glu Asp Ser Ile Ser Gln Gly Pro Val Cys Asn Lys Asn  
 340 345 350

Gly Ser

<210> 24  
 <211> 1062  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> cDNA sequence of clone pC3-hEDG5#3.4 from the region encoding a  
 hEDG5 polypeptide

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<210> 25

<211> 1062

<212> DNA

<213> Artificial Sequence

<220>

<223> cDNA sequence of clone pC3-hEDG5#28 from the region encoding a hEDG5 polypeptide

<400> 25

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actgtcgatg actggacagg aacaaagctt gtgattgttt tgtgtgttgg gacgtttttc	120
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ctggttatcg ccgtggagag gcacatgtca atcatgagga tgcgggtcca tagcaacctg	420
acaaaaaaga gggtgacact gctcattttg cttgtctggg ccatcgccat ttttatgggg	480
gcggtcccca cactgggctg gaattgcctc tgcaacatct ctgcctgctc ttccctggcc	540
gccatttaca gcaggagtta cttgtttttc tggacagtgt ccaacctcat ggccttcctc	600
atcatggttg tgggtgtacct gcggatctac gtgtacgtca agaggaaaac caacgtcttg	660
tctccgcata caagtgggtc catcagccgc cggaggacac ccatgaagct aatgaagacg	720
gtgatgactg tcttaggggc gtttgtggta tgctggaccc cgggcctggg ggttctgctc	780
ctcgacggcc tgaactgcag gcagtgtggc gtgcagcatg tgaaaagggtg gttcctgctg	840
ctggcgctgc tcaactccgt cgtgaacccc atcatctact cctacaagga cgaggacatg	900
tatggcacca tgaagaagat gatctgctgc ttctctcagg agaaccaga gaggcgtccc	960

tctcgcatcc cctccacagt cctcagcagg agtgacacag gcagccagta catagaggat 1020  
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<210> 26  
 <211> 1523  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Complementary strand nucleotide sequence of the genomic DNA  
 flanking 5' end of the hedg-5 cDNA insert of pC3-hedg-55 clone  
 and the hedg-5 cDNA

<400> 26  
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 tgaagtccag aagttgaggg aactaccctc aatcgggtctt gcccgaaatct ttgtcgttaa 180  
 ctaccgaatc actgactaaa atgtttacta taaacaaaga agaaatttaa agaaagatcc 240  
 tacaagtga gaagaggtgt tacttactca cagtgatact gttcgtgtac ctgaaaaaaaa 300  
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 acacacaacc ctgcaaaaag acggacaaat aaaaaaaaaag attaagagac cagtagcgcc 420  
 gtcactagtt tttgtctttt aaagtaaagg ggaaaatgat ggacaaccga ttaaactcgac 480  
 gacggctaaa gaagcgacct taacggatac ataaggacta caaattgtgt ccgggtcaaa 540  
 gtttttgaaa ctgacagttg gcgaccaaag aggcagtccc cgaagacctg tcatcgaact 600  
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 acgcccaggt atcgttggac tggtttttct cccactgtga cgagtaaaac gaacagaccc 720  
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tcttgggtct ctccgcaggg agagcgtagg ggaggtgtca ggagtcgtcc tcaactgtgtc 1260  
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 taatggacag agattgtttc gggtagatgt cacaataaac tccagaggta attagtgacg 1440  
 atctaaagaa attttttaaa aaaaagtatc aaattttcgt acccgtcatt tctctcctgg 1500  
 acgacgtaaa tctctttcgt gtc 1523

<210> 27  
 <211> 353  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Predicted amino acid sequence of hEDG5 encoded by clone  
 pC3-hEDG5#3.4

<400> 27

Met Asn Glu Cys His Tyr Asp Lys His Met Asp Phe Phe Tyr Asn Arg  
 1 5 10 15

Ser Asn Thr Asp Thr Val Asp Asp Trp Thr Gly Thr Lys Leu Val Ile  
 20 25 30

Val Leu Cys Val Gly Thr Phe Phe Cys Leu Phe Ile Phe Phe Ser Asn  
 35 40 45

Ser Leu Val Ile Ala Ala Val Ile Lys Asn Arg Lys Phe His Phe Pro  
 50 55 60

Phe Tyr Tyr Leu Leu Ala Asn Leu Ala Ala Asp Phe Phe Ala Gly  
 65 70 75 80

Ile Ala Tyr Val Phe Leu Met Phe Asn Thr Gly Pro Val Ser Lys Thr  
 85 90 95

Leu Thr Val Asn Arg Trp Phe Leu Arg Gln Gly Leu Leu Asp Ser Ser  
 100 105 110

Leu Thr Ala Ser Leu Thr Asn Leu Leu Val Ile Ala Val Glu Arg His  
 115 120 125

Met Ser Ile Met Arg Met Arg Val His Ser Asn Leu Thr Lys Lys Arg  
 130 135 140

Val Thr Leu Leu Ile Leu Leu Val Trp Ala Ile Ala Ile Phe Met Gly  
 145 150 155 160

Ala Val Pro Thr Leu Gly Trp Asn Cys Leu Cys Asn Ile Ser Ala Cys  
 165 170 175

Ser Ser Leu Ala Pro Ile Tyr Ser Arg Ser Tyr Leu Val Phe Trp Thr  
 180 185 190

Val Ser Asn Leu Met Ala Phe Leu Ile Met Val Val Val Tyr Leu Arg  
 195 200 205

Ile Tyr Val Tyr Val Lys Arg Lys Thr Asn Val Leu Ser Pro His Thr  
 210 215 220

Ser Gly Ser Ile Ser Arg Arg Arg Thr Pro Met Lys Leu Met Lys Thr  
 225 230 235 240

Val Met Thr Val Leu Gly Ala Phe Val Val Cys Trp Thr Pro Gly Leu  
 245 250 255

Val Val Leu Leu Leu Asp Gly Leu Asn Cys Arg Gln Cys Gly Val Gln  
 260 265 270

His Val Lys Arg Trp Phe Leu Leu Leu Ala Leu Leu Asn Ser Val Val  
 275 280 285

Asn Pro Ile Ile Tyr Ser Tyr Lys Asp Glu Asp Met Tyr Gly Thr Met  
 290 295 300

Lys Lys Met Ile Cys Cys Phe Ser Gln Glu Asn Pro Glu Arg Arg Pro  
 305 310 315 320

Ser Arg Ile Pro Ser Thr Val Leu Ser Arg Ser Asp Thr Gly Ser Gln  
 325 330 335

Tyr Ile Glu Asp Ser Ile Ser Gln Gly Ala Val Cys Asn Lys Ser Thr

340

345

350

Ser

&lt;210&gt; 28

&lt;211&gt; 353

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Predicted amino acid sequence of hEDG5 encoded by clone  
pC3-hEDG5#28

&lt;400&gt; 28

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Gly	Asn	Thr	Asp	Thr	Val	Asp	Asp	Trp	Thr	Gly	Thr	Lys	Leu	Val	Ile
			20					25					30		

Val	Leu	Cys	Val	Gly	Thr	Phe	Phe	Cys	Leu	Phe	Ile	Phe	Phe	Ser	Asn
		35					40					45			

Ser	Leu	Val	Ile	Ala	Ala	Val	Ile	Lys	Asn	Arg	Lys	Phe	His	Phe	Pro
	50					55					60				

Phe	Tyr	Tyr	Leu	Leu	Ala	Asn	Leu	Ala	Ala	Ala	Asp	Phe	Phe	Ala	Gly
65					70					75					80

Ile	Ala	Tyr	Val	Phe	Leu	Met	Phe	Asn	Thr	Gly	Pro	Val	Ser	Lys	Thr
				85					90					95	

Leu	Thr	Val	Asn	Arg	Trp	Phe	Leu	Arg	Gln	Gly	Leu	Leu	Asp	Ser	Ser
			100					105					110		

Leu	Thr	Ala	Ser	Leu	Thr	Asn	Leu	Leu	Val	Ile	Ala	Val	Glu	Arg	His
		115					120					125			

Met	Ser	Ile	Met	Arg	Met	Arg	Val	His	Ser	Asn	Leu	Thr	Lys	Lys	Arg
	130					135					140				

Val	Thr	Leu	Leu	Ile	Leu	Leu	Val	Trp	Ala	Ile	Ala	Ile	Phe	Met	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

145		150		155		160
Ala Val Pro Thr	Leu Gly Trp Asn Cys	Leu Cys Asn Ile Ser	Ala Cys			
	165	170	175			
Ser Ser Leu Ala Pro Ile Tyr Ser Arg Ser Tyr Leu Val Phe Trp Thr						
	180	185	190			
Val Ser Asn Leu Met Ala Phe Leu Ile Met Val Val Val Tyr Leu Arg						
	195	200	205			
Ile Tyr Val Tyr Val Lys Arg Lys Thr Asn Val Leu Ser Pro His Thr						
	210	215	220			
Ser Gly Ser Ile Ser Arg Arg Arg Thr Pro Met Lys Leu Met Lys Thr						
	225	230	235			240
Val Met Thr Val Leu Gly Ala Phe Val Val Cys Trp Thr Pro Gly Leu						
	245	250	255			
Val Val Leu Leu Leu Asp Gly Leu Asn Cys Arg Gln Cys Gly Val Gln						
	260	265	270			
His Val Lys Arg Trp Phe Leu Leu Leu Ala Leu Leu Asn Ser Val Val						
	275	280	285			
Asn Pro Ile Ile Tyr Ser Tyr Lys Asp Glu Asp Met Tyr Gly Thr Met						
	290	295	300			
Lys Lys Met Ile Cys Cys Phe Ser Gln Glu Asn Pro Glu Arg Arg Pro						
	305	310	315			320
Ser Arg Ile Pro Ser Thr Val Leu Ser Arg Ser Asp Thr Gly Ser Gln						
	325	330	335			
Tyr Ile Glu Asp Ser Ile Ser Gln Gly Ala Val Cys Asn Lys Ser Thr						
	340	345	350			
Ser						